

## SEQUENCE LISTING

<110> Ip, Nancy Y  
Cheung, William M W

<120> DNA SEQUENCE ENCODING A RETINOIC ACID REGULATED PROTEIN

<130> FP4220B

<150> US 10/409,511

<151> 2003-04-08

<160> 5

<170> PatentIn version 3.2

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<211> 2831

<212> DNA

<213> Homo sapiens

<220>

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cc 120

ctg atg ctc ttc aat tcg gtg ctc cgc cag ccc cag ctt ggc gtc ctg  
168

Met Leu Phe Asn Ser Val Leu Arg Gln Pro Gln Leu Gly Val Leu

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10

15

aga aat gga tgg tct tca caa tac cct ctt caa tcc ctt ctg act ggt.  
216

Arg Asn Gly Trp Ser Ser Gln Tyr Pro Leu Gln Ser Leu Leu Thr Gly

20

25

30

tat cag tgc agt ggt aat gat gaa cac act tct tat gga gaa aca gga  
264

Tyr Gln Cys Ser Gly Asn Asp Glu His Thr Ser Tyr Gly Glu Thr Gly

35

40

45

gtc cca gtt cct cct ttt gga tgt acc ttc tct tct gct ccc aat atg  
312

Val Pro Val Pro Pro Phe Gly Cys Thr Phe Ser Ser Ala Pro Asn Met

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55

60

gaa cat gta cta gca gtt gcc aat gaa gaa ggc ttt gtt cga ttg tat  
360

Glu His Val Leu Ala Val Ala Asn Glu Glu Gly Phe Val Arg Leu Tyr

65

70

75

aac aca gaa tca caa agt ttc aga aag aag tgc ttc aaa gaa tgg atg  
408

Asn Thr Glu Ser Gln Ser Phe Arg Lys Lys Cys Phe Lys Glu Trp Met

80

85

90

95

gct cac tgg aat gcc gtc ttt gac ctg gcc tgg gtt cct ggt gaa ctt  
456

Ala His Trp Asn Ala Val Phe Asp Leu Ala Trp Val Pro Gly Glu Leu

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105

110

aaa ctt gtt aca gca gca ggt gat caa aca gcc aaa ttt tgg gac gta  
504

Lys Leu Val Thr Ala Ala Gly Asp Gln Thr Ala Lys Phe Trp Asp Val

115

120

125

aaa gct ggt gag ctg att gga aca tgc aaa ggt cat caa tgc agc ctc  
552

Lys Ala Gly Glu Leu Ile Gly Thr Cys Lys Gly His Gln Cys Ser Leu

130

135

140

aag tca gtt gcc ttt tct aag ttt gag aaa gct gta ttc tgt acg ggt  
600

Lys Ser Val Ala Phe Ser Lys Phe Glu Lys Ala Val Phe Cys Thr Gly

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155

gga aga gat ggc aac att atg gtc tgg gat acc agg tgc aac aaa aaa

648  
 Gly Arg Asp Gly Asn Ile Met Val Trp Asp Thr Arg Cys Asn Lys Lys  
 160 165 170 175  
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 696  
 Asp Gly Phe Tyr Arg Gln Val Asn Gln Ile Ser Gly Ala His Asn Thr  
 180 185 190  
 tca gac aag caa acc cct tca aaa ccc aag aag aaa cag aat tca aaa  
 744  
 Ser Asp Lys Gln Thr Pro Ser Lys Pro Lys Lys Lys Gln Asn Ser Lys  
 195 200 205  
 gga ctt gct cct tct gtg gat ttc cag caa agt gtt act gtg gtc ctc  
 792  
 Gly Leu Ala Pro Ser Val Asp Phe Gln Gln Ser Val Thr Val Val Leu  
 210 215 220  
 ttt caa gac gag aat acc tta gtc tca gca gga gct gtg gat ggg ata  
 840  
 Phe Gln Asp Glu Asn Thr Leu Val Ser Ala Gly Ala Val Asp Gly Ile  
 225 230 235  
 atc aaa gta tgg gat tta cgt aag aat tat act gct tat cga caa gaa  
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 Ile Lys Val Trp Asp Leu Arg Lys Asn Tyr Thr Ala Tyr Arg Gln Glu  
 240 245 250 255  
 ccc ata gca tcc aag tct ttc ctg tac cca ggt agc agc act cga aaa  
 936  
 Pro Ile Ala Ser Lys Ser Phe Leu Tyr Pro Gly Ser Ser Thr Arg Lys  
 260 265 270  
 ctt gga tat tca agt ctg att ttg gat tcc act ggc tct act tta ttt  
 984  
 Leu Gly Tyr Ser Ser Leu Ile Leu Asp Ser Thr Gly Ser Thr Leu Phe

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gct aat tgc aca gac gat aac atc tac atg ttt aat atg act ggg ttg		
1032		
Ala Asn Cys Thr Asp Asp Asn Ile Tyr Met Phe Asn Met Thr Gly Leu		
290	295	300
aag act tct cca gtg gct att ttc aat gga cac cag aac tct acc ttt		
1080		
Lys Thr Ser Pro Val Ala Ile Phe Asn Gly His Gln Asn Ser Thr Phe		
305	310	315
tat gta aaa tcc agc ctt agt cca gat gac cag ttt tta gtc agt ggc		
1128		
Tyr Val Lys Ser Ser Leu Ser Pro Asp Asp Gln Phe Leu Val Ser Gly		
320	325	330
tca agt gat gaa gct gcc tac ata tgg aag gtc tcc aca ccc tgg caa		
1176		
Ser Ser Asp Glu Ala Ala Tyr Ile Trp Lys Val Ser Thr Pro Trp Gln		
340	345	350
cct cct act gtg ctc ctg ggt cat tct caa gag gtc acg tct gtg tgc		
1224		
Pro Pro Thr Val Leu Leu Gly His Ser Gln Glu Val Thr Ser Val Cys		
355	360	365
tgg tgt cca tct gac ttc aca aag att gct acc tgt tct gat gac aat		
1272		
Trp Cys Pro Ser Asp Phe Thr Lys Ile Ala Thr Cys Ser Asp Asp Asn		
370	375	380
aca cta aaa atc tgg cgc ttg aat aga ggc tta gag gag aaa cca gga		
1320		
Thr Leu Lys Ile Trp Arg Leu Asn Arg Gly Leu Glu Glu Lys Pro Gly		
385	390	395

ggt gat aaa ctt tcc acg gtg ggt tgg gcc tct cag aag aaa aaa gag  
1368

Gly Asp Lys Leu Ser Thr Val Gly Trp Ala Ser Gln Lys Lys Lys Glu

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410

415

tca aga cct ggc cta gta aca gta acg agt agc cag agt act cct gcc  
1416

Ser Arg Pro Gly Leu Val Thr Val Thr Ser Ser Gln Ser Thr Pro Ala

420

425

430

aaa gcc ccc agg gta aag tgc aat cca tcc aat tct tcc ccg tca tcc  
1464

Lys Ala Pro Arg Val Lys Cys Asn Pro Ser Asn Ser Ser Pro Ser Ser

435

440

445

gca gct tgt gcc cca agc tgt gct gga gac ctc cct ctt cct tca aat  
1512

Ala Ala Cys Ala Pro Ser Cys Ala Gly Asp Leu Pro Leu Pro Ser Asn

450

455

460

act cct acg ttc tct att aaa acc tct cct gcc aag gcc cgg tct ccc  
1560

Thr Pro Thr Phe Ser Ile Lys Thr Ser Pro Ala Lys Ala Arg Ser Pro

465

470

475

atc aac aga aga ggc tct gtc tcc tcc gtc tct ccc aag cca cct tca  
1608

Ile Asn Arg Arg Gly Ser Val Ser Ser Val Ser Pro Lys Pro Pro Ser

480

485

490

495

tct ttc aag atg tcg att aga aac tgg gtg acc cga aca cct tcc tca  
1656

Ser Phe Lys Met Ser Ile Arg Asn Trp Val Thr Arg Thr Pro Ser Ser

500

505

510

tca cca ccc atc act cca cct gct tcg gag acc aag atc atg tct ccg  
1704

Ser Pro Pro Ile Thr Pro Pro Ala Ser Glu Thr Lys Ile Met Ser Pro

515	520	525
aga aaa gcc ctt att cct gtg agc cag aag tca tcc caa gca gag gct		
1752		
Arg Lys Ala Leu Ile Pro Val Ser Gln Lys Ser Ser Gln Ala Glu Ala		
530	535	540
tgc tct gag tct aga aat aga gta aag agg agg cta gac tca agc tgt		
1800		
Cys Ser Glu Ser Arg Asn Arg Val Lys Arg Arg Leu Asp Ser Ser Cys		
545	550	555
ctg gag agt gtg aaa caa aag tgt gtg aag agt tgt aac tgt gtg act		
1848		
Leu Glu Ser Val Lys Gln Lys Cys Val Lys Ser Cys Asn Cys Val Thr		
560	565	570
gag ctt gat ggc caa gtt gaa aat ctt cat ttg gat ctg tgc tgc ctt		
1896		
Glu Leu Asp Gly Gln Val Glu Asn Leu His Leu Asp Leu Cys Cys Leu		
580	585	590
gct ggt aac cag gaa gac ctt agt aag gac tct cta ggt cct acc aaa		
1944		
Ala Gly Asn Gln Glu Asp Leu Ser Lys Asp Ser Leu Gly Pro Thr Lys		
595	600	605
tca agc aaa att gaa gga gct ggt acc agt atc tca gag cct ccg tct		
1992		
Ser Ser Lys Ile Glu Gly Ala Gly Thr Ser Ile Ser Glu Pro Pro Ser		
610	615	620
cct atc agt ccg tat gct tca gaa agc tgt gga acg cta cct ctt cct		
2040		
Pro Ile Ser Pro Tyr Ala Ser Glu Ser Cys Gly Thr Leu Pro Leu Pro		
625	630	635

ttg aga cct tgt gga gaa ggg tct gaa atg gta ggc aaa gag aat agt  
2088

Leu Arg Pro Cys Gly Glu Gly Ser Glu Met Val Gly Lys Glu Asn Ser

640 645 650 655

tcc cca gag aat aaa aac tgg ttg ttg gcc atg gca gcc aaa cgg aag  
2136

Ser Pro Glu Asn Lys Asn Trp Leu Leu Ala Met Ala Ala Lys Arg Lys

660 665 670

gct gag aat cca tct cca cga agt ccg tca tcc cag aca ccc aat tcc  
2184

Ala Glu Asn Pro Ser Pro Arg Ser Pro Ser Ser Gln Thr Pro Asn Ser

675 680 685

agg aga cag agc gga aag aca ttg cca agc ccg gtc acc atc acg ccc  
2232

Arg Arg Gln Ser Gly Lys Thr Leu Pro Ser Pro Val Thr Ile Thr Pro

690 695 700

agc tcc atg agg aaa atc tgc aca tac ttc cat aga aag tcc cag gag  
2280

Ser Ser Met Arg Lys Ile Cys Thr Tyr Phe His Arg Lys Ser Gln Glu

705 710 715

gac ttc tgt ggt cct gaa cac tca aca gaa tta tagattctaa tctgagtg  
ag 2333

Asp Phe Cys Gly Pro Glu His Ser Thr Glu Leu

720 725 730

ttactgagct ttgttccact aaaacaagct gagcttttgt ccactaaaac aagatgaa  
aa 2393

atacaagagt gactctataa ctctggtcct taagaaagct gccttttcat ttttagac  
aa 2453

aatcttttca acgctgaaat gtacctaatac tggttctact accataatgt atatgcag  
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tg 2573

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at 2693

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<212> PRT

<213> Homo sapiens

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Gln Cys Ser Gly Asn Asp Glu His Thr Ser Tyr Gly Glu Thr Gly Val

35 40 45

Pro Val Pro Pro Phe Gly Cys Thr Phe Ser Ser Ala Pro Asn Met Glu

50 55 60

His Val Leu Ala Val Ala Asn Glu Glu Gly Phe Val Arg Leu Tyr Asn



65		70		75		80									
Thr	Glu	Ser	Gln	Ser	Phe	Arg	Lys	Lys	Cys	Phe	Lys	Glu	Trp	Met	Ala
			85						90					95	
His	Trp	Asn	Ala	Val	Phe	Asp	Leu	Ala	Trp	Val	Pro	Gly	Glu	Leu	Lys
			100						105					110	
Leu	Val	Thr	Ala	Ala	Gly	Asp	Gln	Thr	Ala	Lys	Phe	Trp	Asp	Val	Lys
			115						120					125	
Ala	Gly	Glu	Leu	Ile	Gly	Thr	Cys	Lys	Gly	His	Gln	Cys	Ser	Leu	Lys
			130						135					140	
Ser	Val	Ala	Phe	Ser	Lys	Phe	Glu	Lys	Ala	Val	Phe	Cys	Thr	Gly	Gly
145									150					155	160
Arg	Asp	Gly	Asn	Ile	Met	Val	Trp	Asp	Thr	Arg	Cys	Asn	Lys	Lys	Asp
									165					170	175
Gly	Phe	Tyr	Arg	Gln	Val	Asn	Gln	Ile	Ser	Gly	Ala	His	Asn	Thr	Ser
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Asp	Lys	Gln	Thr	Pro	Ser	Lys	Pro	Lys	Lys	Lys	Gln	Asn	Ser	Lys	Gly
									195					200	205

Leu Ala Pro Ser Val Asp Phe Gln Gln Ser Val Thr Val Val Leu Phe  
 210 215 220

Gln Asp Glu Asn Thr Leu Val Ser Ala Gly Ala Val Asp Gly Ile Ile  
 225 230 235 240

Lys Val Trp Asp Leu Arg Lys Asn Tyr Thr Ala Tyr Arg Gln Glu Pro  
 245 250 255

Ile Ala Ser Lys Ser Phe Leu Tyr Pro Gly Ser Ser Thr Arg Lys Leu  
 260 265 270

Gly Tyr Ser Ser Leu Ile Leu Asp Ser Thr Gly Ser Thr Leu Phe Ala  
 275 280 285

Asn Cys Thr Asp Asp Asn Ile Tyr Met Phe Asn Met Thr Gly Leu Lys  
 290 295 300

Thr Ser Pro Val Ala Ile Phe Asn Gly His Gln Asn Ser Thr Phe Tyr  
 305 310 315 320

Val Lys Ser Ser Leu Ser Pro Asp Asp Gln Phe Leu Val Ser Gly Ser  
 325 330 335

Ser Asp Glu Ala Ala Tyr Ile Trp Lys Val Ser Thr Pro Trp Gln Pro  
 340 345 350

Pro Thr Val Leu Leu Gly His Ser Gln Glu Val Thr Ser Val Cys Trp  
 355 360 365

Cys Pro Ser Asp Phe Thr Lys Ile Ala Thr Cys Ser Asp Asp Asn Thr  
 370 375 380

Leu Lys Ile Trp Arg Leu Asn Arg Gly Leu Glu Glu Lys Pro Gly Gly  
 385 390 395 400

Asp Lys Leu Ser Thr Val Gly Trp Ala Ser Gln Lys Lys Lys Glu Ser  
 405 410 415

Arg Pro Gly Leu Val Thr Val Thr Ser Ser Gln Ser Thr Pro Ala Lys  
 420 425 430

Ala Pro Arg Val Lys Cys Asn Pro Ser Asn Ser Ser Pro Ser Ser Ala  
 435 440 445

Ala Cys Ala Pro Ser Cys Ala Gly Asp Leu Pro Leu Pro Ser Asn Thr  
 450 455 460

Pro Thr Phe Ser Ile Lys Thr Ser Pro Ala Lys Ala Arg Ser Pro Ile  
 465 470 475 480

Asn Arg Arg Gly Ser Val Ser Ser Val Ser Pro Lys Pro Pro Ser Ser

485	490	495
Phe Lys Met Ser Ile Arg Asn Trp Val Thr Arg Thr Pro Ser Ser Ser		
500	505	510
Pro Pro Ile Thr Pro Pro Ala Ser Glu Thr Lys Ile Met Ser Pro Arg		
515	520	525
Lys Ala Leu Ile Pro Val Ser Gln Lys Ser Ser Gln Ala Glu Ala Cys		
530	535	540
Ser Glu Ser Arg Asn Arg Val Lys Arg Arg Leu Asp Ser Ser Cys Leu		
545	550	555
Glu Ser Val Lys Gln Lys Cys Val Lys Ser Cys Asn Cys Val Thr Glu		
565	570	575
Leu Asp Gly Gln Val Glu Asn Leu His Leu Asp Leu Cys Cys Leu Ala		
580	585	590
Gly Asn Gln Glu Asp Leu Ser Lys Asp Ser Leu Gly Pro Thr Lys Ser		
595	600	605
Ser Lys Ile Glu Gly Ala Gly Thr Ser Ile Ser Glu Pro Pro Ser Pro		
610	615	620

Ile Ser Pro Tyr Ala Ser Glu Ser Cys Gly Thr Leu Pro Leu Pro Leu  
 625 630 635 640

Arg Pro Cys Gly Glu Gly Ser Glu Met Val Gly Lys Glu Asn Ser Ser  
 645 650 655

Pro Glu Asn Lys Asn Trp Leu Leu Ala Met Ala Ala Lys Arg Lys Ala  
 660 665 670

Glu Asn Pro Ser Pro Arg Ser Pro Ser Ser Gln Thr Pro Asn Ser Arg  
 675 680 685

Arg Gln Ser Gly Lys Thr Leu Pro Ser Pro Val Thr Ile Thr Pro Ser  
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Phe Cys Gly Pro Glu His Ser Thr Glu Leu  
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 <213> Homo sapiens

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Thr Pro Asn Ser Arg Arg Gln Ser Gly  
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<210> 5  
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Thr Gly Tyr Gln Cys Ser Gly Asn Asp Glu His Thr Ser Tyr Gly Glu  
 1 5 10 15

Thr Gly Val Pro Val Pro Pro Phe Gly  
 20 25